

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:40:41 ; Search time 12.0465 Seconds
(Without alignments)
837.928 Million cell updates/sec

Title: US-09-622-613B-6

Perfect score: 583

Sequence: 1 MDMLTFQKKHLNTRDVC.....TFCVTCENQAPVHFVGVC 105

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	94.9	104	2 A39035	ribonuclease-relat
2	289	49.6	111	2 A27121	ribonuclease-relat
3	285.5	49.0	111	1 JX0120	ribonuclease-relat
4	269.5	46.2	111	2 JX0085	pancreatic ribonuc
5	149	25.6	119	2 S41111	pancreatic ribonuc
6	131	22.5	124	1 NR01	angiotensin [valida
7	128	22.0	125	1 A32474	pancreatic ribonuc
8	126	21.6	128	1 NRCU	pancreatic ribonuc
9	125	21.4	128	1 NRMK	pancreatic ribonuc
10	120	20.6	128	1 NRKS	pancreatic ribonuc
11	119.5	20.5	145	1 A35932	angiotensin precurs
12	119	20.4	128	1 NRGP	pancreatic ribonuc
13	117	20.1	124	1 NRCB	pancreatic ribonuc
14	116	19.9	125	1 B43825	angiotensin - rabbi
15	116	19.9	128	1 NRY	pancreatic ribonuc
16	114	19.6	124	1 NRHP	angiotensin precurs
17	113	19.4	147	1 NRHAG	pancreatic ribonuc
18	112	19.2	124	1 NRBO	pancreatic ribonuc
19	112	19.2	124	1 NRBO	pancreatic ribonuc
20	112	19.2	124	2 JCS560	pancreatic ribonuc
21	112	19.2	124	2 JCS560	pancreatic ribonuc
22	111.5	19.1	147	2 TS2489	pancreatic ribonuc
23	111	19.0	124	2 NRHO	pancreatic ribonuc
24	111	19.0	128	1 NRHO	pancreatic ribonuc
25	111	19.0	128	1 NRPO	pancreatic ribonuc
26	111	19.0	167	2 S20066	pancreatic-type ri
27	110.5	19.0	123	1 A43825	angiotensin - pig
28	110.5	19.0	155	2 JC6159	eosinophil-associa
29	109	18.7	124	1 NRSH	pancreatic ribonuc

30	109	18.7	124	1 NRPR	pancreatic ribonuc
31	109	18.7	124	1 NRGA	pancreatic ribonuc
32	109	18.7	124	2 S07141	pancreatic ribonuc
33	108	18.5	124	1 NRMB	pancreatic ribonuc
34	108	18.5	124	1 NRGF	pancreatic ribonuc
35	107	18.4	124	1 NRGF	pancreatic ribonuc
36	106	18.2	156	2 JC6160	eosinophil-associa
37	105	18.0	124	1 NRDE	pancreatic ribonuc
38	105	18.0	124	1 NRCM	pancreatic ribonuc
39	105	18.0	124	1 NRCM	pancreatic ribonuc
40	105	18.0	124	1 NRCM	pancreatic ribonuc
41	105	18.0	128	1 NRW2	pancreatic ribonuc
42	104	17.8	124	1 NRY	pancreatic ribonuc
43	103	17.7	124	1 NRDR	pancreatic ribonuc
44	103	17.7	124	1 NRDR	pancreatic ribonuc
45	103	17.7	124	1 NREK	pancreatic ribonuc

ALIGNMENTS

RESULT 1

A39035 ribonuclease-related anti-tumor protein - northern leopard frog (fragment)

C:Species: Rana pipiens (northern leopard frog)

C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993

C:Accession: A39035

R:Ardelet, W., Mikulski, S.M., Shogen, K.

J. Biol. Chem. 266, 245-251, 1991

A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and e

A:Reference number: A39035; MUID:91093131; PMID:1985896

A:Accession: A39035

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-104 <ARD>

C:Superfamily: pancreatic ribonuclease

Query Match 94.9%; Score 553; DB 2; Length 104;

Best Local Similarity 95.2%; Pred. No. 1.1e-48;

Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 QDWLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFTYSRPEPKAICKGIASKNVLT 61

Db 1 EDMLTFQKKHITNTRDVCNNIMSTNLFHCKDKNTFTYSRPEPKAICKGIASKNVLT 60

QY 62 SEFTLSDCNVTSRRCCKKLLKSTNTFCVTCENQAPVHFVGVC 105

Db 61 SEFTLSDCNVTSRRCCKKLLKSTNTFCVTCENQAPVHFVGVC 104

RESULT 2

A27121 ribonuclease-related sialic acid-binding lectin - bullfrog

C:Species: Rana catesbeiana (bullfrog)

C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993

C:Accession: A27121

R:Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawachi, H.; Takayan

A:Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana

A:Reference number: A27121; MUID:87299649; PMID:3304421

A:Accession: A27121

A:Molecule type: protein

A:Residues: 1-111 <RTT>

C:Superfamily: pancreatic ribonuclease

Query Match 49.6%; Score 289; DB 2; Length 111;

Best Local Similarity 48.6%; Pred. No. 4.4e-22;

Matches 54; Conservative 17; Mismatches 32; Indels 8; Gaps 3;

QY 2 QDWLTFQKKHLNTRDVCNNIMSTNLF---HCKDKNTFTYSRPEPKAICKGIASKN 57

Db 1 ENWATEFOCKHILNTRDVCNNIMSTNLF---HCKDKNTFTYSRPEPKAICKGIASKN 59

```
QY      58 VLTSTSEFYISDC---NVTSRPCKKYLKKSTNTFCVTEGNOAPVHVEGVGHG 105
        ||::| | : | ::||| | : || ||||| ||| | : |
Db      60 VLSTRFQLNCTRTISTPRPCPYSSRTEFNVICVKCENQYPVHFAGIGRC 110
```

RESULT 3

ribonuclease-related sialic acid-binding lectin - Japanese frog
C:Species: Rana japonica (Japanese frog)
C:Date: 10-Sep-1999 #sequence,revision 10-Sep-1999 #text,change 10-Sep-1999
C:Accession: JX0120
R:Kamiya, Y.; Oyama, F.; Sakakibara, F.; Nitta, K.; Kawachi, H.; Takayanagi, A.
J. Biochem. 108, 139-143, 1990
A:Title: Amino acid sequence of a lectin from Japanese frog (*Rana japonica*) eggs.
A:Reference number: JX0120; MUID:9105319; PMID:2229005

A:Accession: JX0120
A:Molecule type: protein
A:Residues: 1-111 <RAM>
A:Experimental source: egg
C:Superfamily: pancreatic ribonuclease
K:Keywords: leucin; pyroglutamic acid
F:1.Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:15-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Query Match	49.0%	Pred. 265.5	DB 1	Length 111
Best Local Similarity	45.0%	Pred. No. 9.8e-22		
Matches	50	Conservative 19	Mismatches 35	Indels 7
				Gaps 2

[illegible]

```
OY      38 VLTSTSEFYSDC---NVTSRPCKKYLKKSTNTFCVTCENQAPVHVEGVGHC 105
        |||::||::|   |||::||::|   |||::|||::|   |||::|
Db      61 VLSTTRFQLNTCIRSATAPRCPYNSTRTEFNVICVKCKENRLPVHAGIGRC 111
```

RESULT 4

Pancreatic ribonuclease (EC 3.1.27.5) - bullfrog
 C:Species: *Rana catesbeiana* (bullfrog)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
 C:Accession: JX0085
 R:Nitta, R.; Katsuyama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Onogi, J. *Biochem.* 106, 729-735, 1989
 A:Title: Primary structure of a ribonuclease from bullfrog (*Rana catesbeiana*) liver.
 #:Reference number: JX0085; MUID:50130374; PMID:2613662

C_keywords: hydrolase; pyroglutamic acid
F:10,35,104/modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10,35,104/active site: His_Lys, His #status predicted
F:19-72,34-82,52-97,94-111/Disulfide bonds: #status predicted

Query Match	46.2%	Score 269.5	DB 2	Length 111
Best Local Similarity	43.2%	Pred. No. 4e-20		
Matches 48; Conservative	19	Mismatches 37	Indels 7	Gaps 2

Dy 2 QDMLTFQKAILNTNRDVDCNNIMSTNLF---HCKDKNTFIYSRREPVAICGKIATASKN 57
| | :
Db 1 QNAKFKEKHIRSTSSIDCNIIMDKALYIVCGCKCKERNTFIISSEDNVKAICSGVSPDRK 60

Dy 58 VLTSEFYISDC---NVTSRPCKKYLKKSTNTFCVTCENQAPVAHVGVGHC 105
| : | : | :: | | | | | | | | |
Db 61 ELSTTSFKUNTCIRDSITPRPCYHHPSPDNKKICVKCEKQLPVHEVGIGKC 111

RESULT 5

S41111
pancreatic ribonuclease - common iguana

C:Species: Iguana iguana (common iguana)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #extl_change 21-Aug-1998
C:Accession: S4111
R:Zhao, W., Beintema, J. J., Hofstraenge, J.,
Eur. J. Biochem. 219, 641-646, 1994
A:Title: The amino acid sequence of Iguana (Iguana iguana) pancreatic ribonuclease.
Reference number: S4111; MID:94139745; PMID:8307028

A;Molecule type: protein
A;Residues: 1-119 <ZHA>
C;Superfamily: pancreatic

Query Match	25.68;	Score 149;	DB 2;	Length 119;
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Matches	35;	Conservative	19;	Mismatches	44;	Indels	16;	Gaps	5;
Oy	2	QDLITDQKHL-----	TNTRFDVDCNNIM---	STNLFHCKRCKNNFIYSR	PEPPVA	AI-C	-K	50	
			::: : :		:	:	:		
Db	1	QDMSFQKRLDIPETSA	SNAPAYCDLDMQARRNL	APTRCKRNFVFVAHS	PSPEIDQV	CGSG	60		
			::: : :		:	:	:		
Oy	51	GIASKNVLTSE-FYLSDC---	NVTSRPCKYKLRKSTNTE	FCVTCENQ	ADPVHF	99			
			::: : :		:	:	:		
Db	61	GTHYEDNLVYSNSEFDL	LTDCNNVGATAPSSCK	YMGTRPTKRIIRACEN	ENQVHF	114			
			::: : :		:	:	:		

RESULT 6

pancreatic ribonuclease (EC 3.1.27.5) - culs
N:Alternate names: RNase 1, RNase A
C:Species: *Galea musteloides* (culs)
C:Date: 03-Aug-1994 #sequence_revision 03-Aug-1994 #text_change 04-Oct-1996
C:Accession: A00837
R:Belintema, J.J.; Neuteboom, B.
J.Mol. Evol. 19, 145-152, 1983
A:Title: Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the
A:Reference number: A92957; MUID:87036770; PMID:6571219
A:Accession: A00837

A:Note: about one-third of the molecules lacked Ala-1
C:Comment: The cuts is a rodent belonging to the same subfamily as the guinea pig
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
E:12,41,119/Active site: His, Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:94/Binding site:carboxylate (bsn) (covalent) #status absent

Query Match	22.5%	Score 131;	DB 1;	Length 124;
Best Local Similarity	30.6%	Pred. No.	3.8e-06;	
Matches 37;	Conservative 18;	Mismatches 34;	Indels 32;	Gaps 7;

QY 5 LTFQKKHL-----TNTRDVDCNNIM--STNLHFCKDKNTFIYSRPEPKAICGIIA 54
: ||:: || | | | | :
Db 6 MKFQOQHMDSGHPDTNIN--YCNEMYNRSMIQGRCKRVNTFEHLEPLAVQAVC----S 59

QY 55 SKNV-----LTTSEFLSDCNVTSRP---CKYKLRKSTNIFCVTCEN--QAPVH 98
||| :|| :||| ||| :|| :|| :||| |||
Db 60 QKNVPCKNQTCYQSHSSMRITDCRVTSSSKYPNCSYRMQQAQKSLIVACEGTPSYPVH 119

QY	99	F	99
Db	120	F	120

RESULT 7

angiogenin [validated] - bovine
 N:Alternate names: angiogenesis factor
 N:Contains: ribonuclease (EC 3.1.27.-)
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 25-Sep-1989 #sequence_revision 25-Sep-1989 #text_change 15-Sep-2000
 #Accession: A32474; S02001; A30044; S48212

R:Bond, M.D.; Strydom, D.J.
Biochemistry 28, 6110-6113, 1989

A>Title: Amino acid sequence of bovine angiotensin.

A:Reference number: A32474; PMID:89375344; PMID:2775757

A:Accession: A32474

A:Molecule type: protein

A:Residues: 1-125 <BON>

A:Experimental source: plasma

R:Maes, P., Damart, D.; Rommens, C.; Montreuil, J.; Spik, G.; Tartar, A.
FEBS Lett. 241, 41-45, 1988

A>Title: The complete amino acid sequence of bovine milk angiotensin.

A:Reference number: S02001; PMID:89065101; PMID:3197838

A:Accession: S02001

A:Molecule type: protein

A:Residues: 1-125 <MAE>

A:Experimental source: milk

R:Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
submitted to the Brookhaven Protein Data Bank, January 1995

A:Reference number: A65065; PDB:IAGI

A:Contents: annotation: X-ray crystallography, 1.5 angstroms, residues 1-125

R:Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
Proc. Natl. Acad. Sci. U.S.A. 92, 2949-2953, 1995

A>Title: Crystal structure of bovine angiotensin at 1.5 Angstroms resolution.

A:Reference number: A58315; PMID:95224057; PMID:7708754

A:Contents: annotation: X-ray crystallography, 1.5 angstroms

R:Legin, O.; Albarret, C.; Bonlems, F.; Spik, G.; Lallemand, J.Y.
submitted to the Brookhaven Protein Data Bank, April 1996

A:Reference number: A65709; PDB:IGIO

A:Contents: annotation: conformation by (1)H-NMR, residues 1-125

R:Legin, O.; Albarret, C.; Bonlems, F.; Spik, G.; Lallemand, J.Y.
Biochemistry 35, 8870-8880, 1996

A>Title: Solution structure of bovine angiotensin by (1)H nuclear magnetic resonance spectroscopy.

A:Reference number: A58821; PMID:96280645; PMID:8684423

A:Contents: annotation: conformation by (1)H-NMR

R:Reisdorf, C.; Abbergel, D.; Bonlems, F.; Lallemand, J.Y.; Decotignies, J.P.; Spik, G.
Eur. J. Biochem. 224, 811-822, 1994

A>Title: Proton resonance assignments and secondary structure of bovine angiotensin.

A:Reference number: S48212; PMID:95010071; PMID:7925406

A:Contents: annotation: conformation by (1)H-NMR

C:function:

A>Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues

C:superfamily: pancreatic ribonuclease

C:key words: angiogenesis; hydrolase; nucleic acid degradation

F:60-68/region: receptor binding #status predicted
F:14_41 /His/Active site: His, Tyr, His #status predicted
F:27-82_40-93,58-108/Dissulfide bonds: #status experimental

```
Query Match          22.0%   Score 128; DB 1; Length 125;  
Best Local Similarity    34.0%; Pred. No. 7,7e+06;  
Matches      33; Conservative     14; Mismatches       32; Indels        18; Gaps         5;
```

OY 17 DVDCKNNINSLNF--HKDKNTFFISREPEPYAICKGIASKN-----VLTNSEFL 66
 | :|:| | |||||:| ::|||:
Db 24 DEYCENNAKRNRLTLPCKDRMTFTFGNKNDIAITE----DRNGQPIRGLRIKSERFOI 79
 :|::|||:| * : : : | || | ||
OY 67 SDG---NWTSR-PCKRYLKLKSTNYTCVCENAPAHF 99
 :|:|||:| | : : : | || | ||
Db 80 TICKKHGGSSRPCCRYCATEDSRVIYGCENLPLPVHF 116
 :|:|||:| | : : : | || | ||

RESULT 8
NRCD
pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)
N:Alternate names: RNase 1; RNase A
C:Species: Myocastor coypus (nutria, coypu)
C>Date: 24-Apr-1984 #sequence=revision 30-Sep-1988 #text_change 31-Mar-2000
C:Accession: A00822
R:van den Berg, A.; van den Hende-Timmer, L.; Bentema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A>Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
A:Reference number: A90612; PMID:77065676; PMID:999896
A:Accession: A00822
A:Molecule type: proteain

A:Residues: 1-128 <AN>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
E:12,41,119/Active site: His, Lys, His #status predicted
F:126-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 21.6%; Score 126; DB 1; Length 128;
Best Local Similarity 29.9%; Pred. No. 1.3e-05;
Matches 35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;

OY 7 FOKKHL-----TNRDVCNNIM-STNLF--HCKDKMTFIYSRPEPKAICKGIATSKNV 58
|:::| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 8 FERHMDSRGSPSTINPNVNCNMEMKSRMNTGCRCKRPVTFTFHEPLADQAVC----FKKNV 63
| : : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 59 L-----TTSEFYISDCNVTSRP---CKYLKKSTNTEFCVTCENQ--APVHF 99
| : : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 64 LCKNGQTNCYOSNSNMHTDCRVTSNSDPYSCSYRTSQEEKSIYVACEGNPYVPVHF 120
| : : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 9
NRMK
pancreatic ribonuclease (EC 3.1.27.5) - minke whale
N:Alternate names: RNase A
C:Species: Balenoptera acutorostrata (minke whale, lesser rorqual)
C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C:Accession: A00818
R:Eimems, M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
A>Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonucle
A:Reference number: A00818; MUID:76277855; PMID:962870
A:Molecule type: protein
A:Residues: 1-124
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
E:12,41,119/Active site: His, Lys, His #status predicted
F:126-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 21.4%; Score 125; DB 1; Length 124;
Best Local Similarity 28.6%; Pred. No. 1.5e-05;
Matches 34; Conservative 15; Mismatches 42; Indels 28; Gaps 6;

OY 5 LTPOKHILTNTRVD-----CNNIMSTFLF---HCKDKMTFIYSRPREPVAKICKGITASK 56
|:::| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 6 MKFOROHMDSGSNSPGNNPNVNYCNOMMMRRKMTOGRCKRPVNTVESLEDPKAVC---SQR 61
| : : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 57 NVL-----TTSEFYISDCNVTSRP---CKYLKKSTNTEFCVTCENQ--APVHF 99
| : : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 62 NVLCKNGTNCYESNSTWHTIDCRQTGSCKRYPCAKRKYSQKEKHIIYACENPRYPVPHF 120
| : : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 10
NRKS
pancreatic ribonuclease (EC 3.1.27.5) - casiragua
C:Species: Proechimys guairae (casiragua)
C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 30-Sep-1993
C:Accession: A00821
R:Beintema, J.J.; Knoll, G.; Martena, B.
Biochim. Biophys. Acta 705, 102-110, 1982
A>Title: The primary structures of pancreatic ribonucleases from African porcupine and
A:Reference number: A00644; MUID:83000399; PMID:7115727
A:Accession: A00821
A:Molecule type: protein
A:Residues: 1-128 <BE>
A>Note: residues 67-78 were positioned primarily by homology with other ribonucleases
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
E:12,41,119/Active site: His, Lys, His #status predicted
F:126-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

```

Query Match 35: 20.6%; Score 120; DB 1; Length 128;
Best Local Similarity 29.9%; Pred. No. 5.1e-05;
Matches 35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;

OY 7 FQKRL-----TNRDVCNNIM-STNLF--HCKDKNFIFSRPEPAICGIIASKNV 58
      |||::|  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 8 FQPHIDSSGSPSTNPVNCNMAKMSRMTQRCRPRVNFVEHPLADQAVC-----FQKNV 63
      |||::|  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||

OY 59 -----LTTSEFYLSDCNVTSR---PCKYKLLKSTNFTFCVCEMO--ADVHF 99
      ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 64 PCKNGOSNCYESTSNMHTDCLRTLSNSKFPDCLYRTSQEEKSIIVACEGNDYVHF 120
      ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||

RESULT 11
A35932
angiotenin precursor - mouse
N:Alternate names: angiotensin factor
N:Contains: ribonuclease (EC 3.1.27.-)
C:Species: Mus musculus (house mouse)
C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
C:Accession: A35932
R:Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A:Title: Isolation and sequencing of mouse angiotenin DNA.
A:Reference number: A35932; MUID:91025023; PMID:2222438
A:Accession: A35932
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-145 <BON>
A:Cross-references: GB:022516; NID:g726325; PIDN:AAA91366.1; PID:g726326
A:Genetics:
A:Introns: #status absent
C:Function:
A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C:Superfamily: pancreatic ribonuclease
C:Keywords: angiotensin; hydrolysis; nucleic acid degradation; pyroglutamic acid
F:1-24/Domin: signal sequence #status predicted <SIG>
F:25-145/Product: angiotenin #status predicted <MAT>
F:25/Modified site: pyroglutamate carboxylic acid (Glu) (in mature form) #status predicted
F:37/64,137/Active site: His, Lys, His #status predicted
F:50-104,63-115,81-130/Disulfide bonds: #status predicted

Query Match 33: 20.5%; Score 119.5; DB 1; Length 145;
Best Local Similarity 30.8%; Pred. NO. 6.5e-05;
Matches 33; Conservative 12; Mismatches 45; Indels 17; Gaps 5;

OY 10 KHLNTPDVD-----CNNINSTNLF--HCKDKNFIFSRPEPAICG--KGIASKN 57
      |||::|  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 32 KFLQGHNDANPKGDDDYECERMMKRRSLTSPCKVNFTHFGNKSNTAICGANGSPREN 91
      |||::|  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||

OY 58 V-LTTSEFYLSDCNVTSR---PCKYKLLKSTNFTFCVCEMOADVHF 99
      ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 92 LRMSKSPFOVTTCKHTGSPRRPCQYRASAGFRHVIACENGDPVHF 138
      ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||

RESULT 12
NRGPB
pancreatic ribonuclease (EC 3.1.27.5) B - guinea pig (tentative sequence)
N:Alternate names: RNase IB
C:Species: Cavia porcellus (guinea pig)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C:Accession: A00826
R:van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gastra, W.; Belintema, J.J.
Eur. J. Biochem. 75, 91-100, 1977
A:Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure
A:Reference number: A91247; MUID:77105023; PMID:862624
A:Accession: A00826
A:Molecule type: protein
A:Residues: 1-128 <VAN>
A:Note: 64-Pro was also found
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,41,119/Active site: His, Lys, His #status predicted

```

F:21_34/Binding site: carbohydrate (asn) (covalent) #status experimental
F:26-84;40-95;58-110;65-72/Dissulfide bonds: #status predicted

Query Match 20.4%; Score 119; DB 1; Length 128;
Best Local Similarity 28.3%; Pred. No. 6,4e+05;
Matches 34; Conservative 21; Mismatches 35; Indels 30; Gaps 7;

Oy 5 LTFQKHL-----TNTRDVDCNNIM---STNLEHCKDKDKNFTYSRPEPKAICKGIITAS 55
 : :::: |::| :||:: ||:::
Db 6 MKFORIHDEGSPSSNSNY-CNVMIIRRNMTQGRCKPVTFFVESLADYQAVC----FQ 60
 : :::: |::| :||:: ||:::

Oy 56 KNLV-----TTSEFYISDCNVIISR--CKTKLKSKTNTPFCYTCENO--APVHF 99
 : :::: |::| :||:: ||:::
Db 61 KNVLCKNGQTNCYOYSRMRTIDCRWTSKSKFPNCGRMSQAOKSIIVACEGPDPVEVHF 120
 : :::: |::| :||:: ||:::

RESULT 13
NRCB
pancreatic ribonuclease (EC 3.1.27.5) - Chinchilla brevicaudata (tentative sequence)
M:Alternate names: RNase 1; RNase A
C:Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata
C>Date: 24-Apr-1984 #sequence_revision 30-sep-1988 #text_change 31-Mar-2000
C:Accession: A00820
R:vander Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A>Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic F:12-41;119/Active site: His, Lys, His #status predicted
E:26-84;40-95;58-110;65-72/Dissulfide bonds: #status predicted
F:34/Binding site: carbohydrate (asn) (covalent) #status experimental

A:Molecule type: protein
A:Residues: 1-124 <VAN>
A>Note: a second component of chinchilla ribonuclease has 32-Asp
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
E:12-41;119/Active site: His, Lys, His #status predicted
F:26-84;40-95;58-110;65-72/Dissulfide bonds: #status predicted
F:34/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 20.1%; Score 117; DB 1; Length 124;
Best Local Similarity 26.9%; Pred. No. 9,8e+05;
Matches 32; Conservative % 19; Mismatches 40; Indels 28; Gaps 6;

Oy 5 LTFQKHL-----TNTRDVDCNNIM---STNLEHCKDKDNFTYSRPEPKAICKGIITASK 56
 : :::: |::| :||:: ||:::
Db 6 MKFORIHMDSSGSPTANANCENMKMRNMTOGYCKPVFNFHEPLADYQAVC---FOK 61
 : :::: |::| :||:: ||:::

Oy 57 NV-----LTSEFYISDCNVIISR--CKTKLKSKTNTPCYTCENO--APVHF 99
 : :::: |::| :||:: ||:::
Db 62 NVECKNQSNCSYOVSNSMMHTTDCKRLTNSKYPRMCSTRSREKGIIYACGNPPVPVHF 120
 : :::: |::| :||:: ||:::

RESULT 14
B43825
angiogenin - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S29833; B43825
R:Bond, M.D.; Strýdom, D.J.; Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
A>Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: discer
A:Reference number: S29833; PMID:93192291; PMID:8448182
A:Accession: S29833
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-125 <RON>
A>Note: submitted to the Protein Sequence Database, December 1992
C:Superfamily: pancreatic ribonuclease
C:Keywords: pyroglutamic acid
F:I/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 19.9%; Score 116; DB 1; Length 125;
Best Local Similarity 31.2%; Pred. No. 0.,00012;
Matches 24; Conservative 13; Mismatches 32; Indels 8; Gaps 3;

QY 31 KCKNFETYSRPEPVARK---GIASKV-VLTSEFLSDONVTS---PRCKYKLLK 82
||| ||| : : : : : ||| : : : : : ||| :
Db 39 CKDINFEVHONKSGIKVCCEDKNKGKPYKGNFRISKSPQYTTCKHGGSGPWPCRRRANS 98
QY 83 STINFCTYCENQAPVHF 99
: : : ||| ||| |||
Db 99 GSRNIVTIACENGCLPVHF 115

